

TABLE 3U Genes Corresponding To Genes Shared as Between Allergies and OA					
Spot	p-value	Clone	Description	Accession	Allergies/No Allergies
10733	0.049555	seoc6410	DKFZp434O0813_s1 434 (synonym: htes3) cDNA clone DKFZp434O0813 3', mRNA sequence /clone=DKFZp434O0813 /clone_end=3'	AL040360	1.22
8860	0.049555	seoc6169	clone 23612 mRNA sequence /gb=U90902	U90902	1.34
13748	0.049555	miod5306	Similar to likely ortholog of yeast ARV1, clone IMAGE:4106796, mRNA /gb=BC018945	BC018945	1.17
13041	0.049555	seoc7820	AGENCOURT_8351558 NIH_MGC_113 cDNA clone IMAGE:6282273 5', mRNA sequence /clone=IMAGE:6282273 /clone_end=5' /gb=BQ706828	BQ706828	1.29
11126	0.049555	miod2852	full length insert cDNA clone ZD64C04 /gb=AF088052 /gi=3523258 /ug=Hs.384557 /len=831	AF088052	1.19
14439	0.049555	seoc5860	cDNA FLJ13571 fis, clone PLACE1008405. /gb=AK023633 /gi=10435617 /ug=Hs.116278	AK023633	1.18
8423	0.049555	ncr8883	ot96g10.s1 Soares_total_fetus_Nb2HF8_9w cDNA clone IMAGE:1624674 3', mRNA sequence /clone=IMAGE:1624674 /clone_end=3' /gb=AA993566	AA993566	1.23
3911	0.049555	ncr2398	mitochondrion, complete genome	NC_001807	0.81
10534	0.049555	miob8515	hypothetical protein DKFZp762A217 (DKFZp762A217), mRNA /cds=(433,2943)	NM_152588	1.20
3702	0.049555	fcr0180	ferritin, heavy polypeptide 1 (FTH1), mRNA /cds=(92,664) /gb=NM_002032 /gi=4503794	NM_002032	1.17
5439	0.049555	ncrc2377	hypothetical protein MGC4276 similar to CG8198 (MGC4276), mRNA /cds=(70,462) /gb=NM_030940	NM_030940	0.87
13423	0.049555	seoa6355	mRNA; cDNA DKFZp686E1027 (from clone DKFZp686E1027) /gb=AL832759 /gi=21733340	AL832759	1.18
14871	0.046607	miod3222	BAC clone RP11-449G3 from 7, complete sequence	AC019210	1.15
12771	0.046607	fcrb5090	cDNA FLJ37324 fis, clone BRAMY2018279. /gb=AK094643 /gi=21753744 /ug=Hs.12714 /len=2844	AK094643	1.28
11770	0.046607	fcr6297	cDNA FLJ33160 fis, clone UTERU2000485. /gb=AK057722 /gi=16553641 /ug=Hs.429349	AK057722	1.25
9623	0.046607	seob9001	KIAA0854 protein (KIAA0854), mRNA /cds=(305,2818) /gb=NM_014943 /gi=7662341	NM_014943	0.85
13280	0.046607	miod5207	cDNA FLJ13792 fis, clone THYRO1000072, weakly similar to MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC	AK023854	1.16
13419	0.046607	miob2317	chromosome 11, clone RP11-4B7, complete	AC026639	1.20
6522	0.046607	seoa2194	Rattus norvegicus mitochondrial genome	NC_001665	0.82
8924	0.046607	ncr8228	BX112599 Soares fetal liver spleen 1NFLS cDNA clone IMAGp998N15537, mRNA sequence /clone=IMAGp998N15537 ; IMAGE:248654	BX112599	1.23
869	0.046607	miob2448	receptor associated protein 80 (RAP80), mRNA /cds=(110,2269) /gb=NM_016290 /gi=21361592	NM_016290	0.76
3456	0.046607	fcrb3217	ionized calcium binding adapter molecule 2 (IBA2), mRNA /cds=(89,541) /gb=NM_031426 /gi=13899240	NM_031426	1.20
2339	0.046607	seoa8501	chemokine (C-C motif) receptor 5 (CCR5), mRNA /cds=(358,1416) /gb=NM_000579 /gi=4502638	NM_000579	0.81
12074	0.046607	seob2033	DNA sequence from clone RP4-687F11 on chromosome 20 Contains the 5' end of the L3MBTL gene for l(3)mbt-like (Drosophila)(DKFZP434N061), a	AL117334	1.15

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Spot	p-value	Clone	Description	Accession	Allergies/No Allergies
2473	0.046607	hfc3514	Pseudoautosomal GTP-binding protein-like (PGPL), mRNA /cds=(330,1541) /gb=NM_012227 /gi=6912587	NM_012227	0.85
4138	0.043803	miod0835	mRNA; cDNA DKFZp451M092 (from clone DKFZp451M092) /gb=AL713650 /gi=19584326	AL713650	0.82
9129	0.043803	miob8376	alpha gene sequence	AF203815	1.33
5920	0.043803	mioa4643	mitochondrion, complete genome	NC_001807	0.82
5889	0.043803	ncrb4439	mRNA for KIAA0640 protein, partial cds. /cds=(1,1813) /gb=AB014540 /gi=3327093	AB014540	0.60
5301	0.043803	seob6836	X-box binding protein 1 (XBP1), mRNA /cds=(49,834) /gb=NM_005080 /gi=14110394 /ug=Hs.149923	NM_005080	0.80
14495	0.043803	ncr5835	DNA sequence from clone RP11-15J10 on	AL512605	1.42
3592	0.043803	ncrc6407	solute carrier family 30 (zinc transporter), member 5 (SLC30A5), mRNA /cds=(202,2499) /gb=NM_022902	NM_022902	1.11
14847	0.043803	seob8705	chromosome 15, clone CTD-2017F17, complete	AC069368	1.30
7462	0.043803	fcrb8121	TRAF family member-associated NFKB activator (TANK), transcript variant 1, mRNA /cds=(159,1436)	NM_004180	1.20
10363	0.043803	mioa1383	Similar to RIKEN cDNA 2310026P19 gene, clone MGC:49935 IMAGE:6175382, mRNA, complete cds	BC043352	1.18
3056	0.043803	ncrc1193	biglycan (BGN), mRNA /cds=(145,1251) /gb=NM_001711 /gi=19718760 /ug=Hs.821 /len=2367	NM_001711	0.83
12903	0.043803	mioc5237	cDNA FLJ33097 fis, clone TRACH2000775. /gb=AK057659 /gi=16553423 /ug=Hs.415317	AK057659	1.31
10346	0.04114	ncrb3258	UI-E-EO1-aiv-e-19-0-UI.s1 UI-E-EO1 cDNA clone UI-E-EO1-aiv-e-19-0-UI 3', mRNA sequence /clone=UI-E-EO1-aiv-e-19-0-UI /clone_end=3' /gb=BU742864	BU742864	0.78
10937	0.04114	fcrb7036	hypothetical protein MGC16384 (MGC16384), mRNA /cds=(450,602) /gb=NM_053048 /gi=16596689	NM_053048	1.23
12104	0.04114	seob0564	helicase-like protein (KIAA2023), mRNA /cds=(399,5378) /gb=NM_173082 /gi=27436872	NM_173082	1.22
14775	0.04114	mioc5256	Chromosome X PAC RPC11-290C9 from the Pieter de Jong PAC library; complete sequence	AC002404	1.28
10954	0.04114	fcrb5418	desmin (DES), mRNA /cds=(81,1490) /gb=NM_001927 /gi=18105049 /ug=Hs.279604	NM_001927	1.36
9641	0.04114	seoc2504	translocase of inner mitochondrial membrane 17 A (yeast) (TIMM17A), mRNA /cds=(8,523)	NM_006335	0.78
14893	0.04114	seoc1714	EST375707 MAGE resequences, MAGH cDNA, mRNA sequence /gb=AW963634 /gi=8153470	AW963634	1.28
9953	0.04114	miob9284	fatty acid binding protein 1, liver (FABP1), mRNA	NM_001443	1.18
4340	0.04114	hfc2686	heat shock 90kDa protein 1, beta (HSPCB), mRNA /cds=(85,2259) /gb=NM_007355 /gi=20149593	NM_007355	0.83
13005	0.04114	miod5329	zx55g04.r1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:446454 5', mRNA sequence /clone=IMAGE:446454 /clone_end=5' /gb=AA203502	AA203502	1.25
8520	0.04114	fcrb4287	chromosome 20 open reading frame 52 (C20orf52), mRNA /cds=(164,403) /gb=NM_080748 /gi=18152784	NM_080748	0.84
8749	0.04114	miod2232	feritin, heavy polypeptide 1 (FTH1), mRNA /cds=(92,664) /gb=NM_002032 /gi=4503794	NM_002032	1.24
10323	0.04114	ner7133	mRNA; cDNA DKFZp434K1115 (from clone DKFZp434K1115); complete cds /cds=(97,2877)	AL136764	0.72

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Spot	p-value	Clone	Description	Accession	Allergies/No Allergies
5434	0.041137	ncrc7127	ATP synthase, H transporting, mitochondrial F0 complex, subunit b, isoform 1 (ATP5F1), mRNA	NM_001688	0.84
11760	0.038612	fcrc4968	arrestin, beta 2 (ARRB2), mRNA /cds=(234,1463) /gb=Nm_004313 /gi=21626464 /ug=Hs.18142	NM_004313	1.17
3273	0.038612	fcrc0456	golgi reassembly stacking protein 2, 55kDa (GORASP2), mRNA /cds=(52,1524) /gb=Nm_015530	NM_015530	0.88
2212	0.038612	mioa4674	chromosome 21 open reading frame 4 (C21orf4), mRNA /cds=(159,635) /gb=Nm_006134 /gi=8659558	NM_006134	0.78
12936	0.038612	mioc4394	clone IMAGE:5263531, mRNA /gb=BC037740	BC037740	0.61
5769	0.038612	miod3065	cDNA: FLJ21561 fis, clone COL06415. /gb=AK025214 /gi=10437681 /ug=Hs.96918 /len=1641	AK025214	0.75
12751	0.038612	ncrc2521	NISC_gj03b10.x1 NCI_CGAP_Pr28 cDNA clone IMAGE:3270498 3', mRNA sequence /clone=IMAGE:3270498 /clone_end=3' /gb=CB048158	CB048158	1.18
14672	0.038612	ncrc9415	12 BAC RP11-7G5 (Roswell Park Cancer Institute	AC007834	1.22
4887	0.038612	ncrc0487	mRNA; cDNA DKFZp434N079 (from clone DKFZp434N079) /gb=AL133591 /gi=6599179	AL133591	0.80
6860	0.038612	ncrc5075	cDNA: FLJ21440 fis, clone COL04389. /gb=AK025093 /gi=10437540 /ug=Hs.218008 /len=1810	AK025093	0.79
8686	0.038612	mioc3798	mRNA; cDNA DKFZp564P016 (from clone DKFZp564P016) /gb=AL049337 /gi=4500118	AL049337	1.37
4402	0.038612	miod3421	putative homeodomain transcription factor 1 (PHTF1), mRNA /cds=(32,2320) /gb=Nm_006608 /gi=5729975	NM_006608	1.21
12568	0.036213	seoc6071	BAC clone RP11-610J23 from 4, complete sequence	AC079858	1.20
12907	0.036213	mioc6243	UI-E-EO0-ahy-j-09-0-UI.r1 UI-E-EO0 cDNA clone UI-E-EO0-ahy-j-09-0-UI 5', mRNA sequence /clone=UI-E-EO0-ahy-j-09-0-UI /clone_end=5' /gb=BM722772	BM722772	0.60
14390	0.036213	seoc1781	BX097880 NCI_CGAP_Thy1 cDNA clone IMAGp998F242841, mRNA sequence /clone=IMAGp998F242841; IMAGE:1133207	BX097880	1.17
10178	0.036213	miob2233	EST382135 MAGE resequences, MAGK cDNA, mRNA sequence /gb=AW970055 /gi=8159900	AW970055	1.19
9270	0.036213	seob9552	602122561F1 NIH_MGC_56 cDNA clone IMAGE:4279766 5', mRNA sequence /clone=IMAGE:4279766 /clone_end=5' /gb=BF668349	BF668349	1.25
12369	0.036213	miob8235	QV3-BN0047-150400-152-h07 BN0047 cDNA, mRNA sequence /gb=AW997115 /gi=8257349	AW997115	1.19
3361	0.036213	seob1144	integrin, beta 8 (ITGB8), mRNA /cds=(681,2990) /gb=Nm_002214 /gi=4504778 /ug=Hs.355722	NM_002214	0.76
1598	0.036213	fcrc5723	troponin I, skeletal, slow (TNNI1), mRNA /cds=(74,637) /gb=Nm_003281 /gi=21361554	NM_003281	0.72
429	0.036213	miod0625	NPD009 protein (NPD009), mRNA /cds=(1327,1677) /gb=Nm_020686 /gi=24476005 /ug=Hs.283675	NM_020686	0.79
4114	0.03394	miob3313	no match		0.87
4614	0.03394	miob2720	repetitive sequence		1.28
9353	0.03394	seob0051	BAC clone RP11-427F2 from 2, complete sequence	AC116050	1.34
13194	0.03394	miob9370	putative serine-rich protein mRNA, partial cds	AF246705	1.34
2141	0.03394	ncrb2400	transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12), mRNA	NM_003205	0.63

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7052	0.03394	seoa7647	SUMO-1-specific protease (SUSP1), mRNA /cds=(1,3339) /gb=NM_015571 /gi=7662311	NM_015571	0.85
7162	0.03394	fcrb3024	protein-O-mannosyltransferase 1 (POMT1), mRNA /cds=(180,2423) /gb=NM_007171 /gi=21361381	NM_007171	0.70
14169	0.03394	ncrc9474	UI-H-EI0-ayg-o-16-0-UI.s1 NCI_CGAP_EI0 cDNA clone UI-H-EI0-ayg-o-16-0-UI 3', mRNA sequence /clone=UI-H-EI0-ayg-o-16-0-UI /clone_end=3'	CA449027	0.59
11031	0.03394	mioc5223	cDNA: FLJ21228 fis, clone COL00739. /gb=AK024881 /gi=10437293 /ug=Hs.306716 /len=1869	AK024881	1.21
658	0.03394	miod3417	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDEL3), transcript variant 1, mRNA /cds=(157,801) /gb=NM_006855	NM_006855	0.56
12378	0.031786	mioc0202	cDNA FLJ31274 fis, clone KIDNE2006334. /gb=AK055836 /gi=16550665 /ug=Hs.351722	AK055836	1.14
2230	0.031786	mioa9630	PMS1 postmeiotic segregation increased 1 (S. cerevisiae) (PMS1), mRNA /cds=(81,2879)	NM_000534	1.24
4518	0.031786	mioa5411	chromosome 11, clone RP11-745E9, complete	AC026269	1.16
5783	0.031786	ncr2408	ATPase inhibitory factor 1 (ATPIF1), mRNA /cds=(52,372) /gb=NM_016311 /gi=20149627	NM_016311	0.86
14250	0.031786	mioc0276	ferritin, light polypeptide (FTL), mRNA /cds=(189,716) /gb=NM_000146 /gi=20149497 /ug=Hs.430150	NM_000146	1.22
14208	0.031786	seob7571	oxysterol-binding protein 1 (OSBP1) mRNA, complete	AF185696	1.11
9581	0.031786	miod7007	partial steerin-1 gene	AJ251973	1.14
5743	0.031786	hfc2367	heme-regulated initiation factor 2-alpha kinase (HRI), mRNA /cds=(63,1955) /gb=NM_014413 /gi=11125767	NM_014413	0.77
4823	0.031786	fcrb3074	SH3-domain GRB2-like endophilin B2 (SH3GLB2), mRNA /cds=(147,1334) /gb=NM_020145	NM_020145	1.89
10594	0.029748	mioc3937	UI-H-EZ1-bbh-j-15-0-UI.s1 NCI_CGAP_Ch2 cDNA clone UI-H-EZ1-bbh-j-15-0-UI 3', mRNA sequence /clone=UI-H-EZ1-bbh-j-15-0-UI /clone_end=3'	BQ575990	1.33
7406	0.029748	fcrb6211	hypothetical protein FLJ14511 (FLJ14511), mRNA /cds=(23,1273) /gb=NM_033087 /gi=14861835	NM_033087	0.67
11551	0.029748	seoa2648	no match		1.21
5290	0.029748	fcrb3016	hypothetical protein FLJ20719 (FLJ20719), mRNA /cds=(402,2213) /gb=NM_017940 /gi=24308174	NM_017940	0.83
1209	0.029748	ncrc5150	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6) (MPP6), mRNA /cds=(300,1922)	NM_016447	0.75
9928	0.029748	mioc1440	LIM domain containing preferred translocation partner in lipoma (LPP), mRNA /cds=(247,2085)	NM_005578	1.19
13811	0.029748	seoc1628	hypothetical protein FLJ20360 (FLJ20360), mRNA /cds=(80,2305) /gb=NM_017782 /gi=8923334	NM_017782	0.82
10026	0.029748	mioc7444	dishevelled associated activator of morphogenesis 1 (DAAM1), mRNA /cds=(126,3362) /gb=NM_014992	NM_014992	1.18
4421	0.029748	ncr3718	sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA /cds=(46,2430) /gb=NM_005065 /gi=19923668	NM_005065	1.14
8308	0.029748	miob2685	chromosome 16 clone RP11-266L9, complete	AC133552	1.22
11912	0.029748	miod5349	hypothetical protein MGC40157 (MGC40157), mRNA /cds=(106,498) /gb=NM_152350 /gi=22748758	NM_152350	1.21
10571	0.029748	mioc7404	alpha gene sequence	AF203815	1.32

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12672	0.029748	ncr9378	hypothetical protein FLJ21032 (FLJ21032), mRNA	NM_024906	1.27
5150	0.02782	seoa1634	HSPC039 protein mRNA, complete cds /cds=(81,329) /gb=AF125100 /gi=5106995 /ug=Hs.406542 /len=1583	AF125100	0.78
3015	0.02782	ncrc0477	mitochondrion, complete genome	NC_001807	0.82
5294	0.02782	seob5711	KIAA0063 gene product (KIAA0063), mRNA /cds=(280,888) /gb=NM_014876 /gi=7661887	NM_014876	0.77
2550	0.02782	ncr3869	uncharacterized bone marrow protein BM042, clone MGC:45580 IMAGE:4447813, mRNA, complete cds	BC035601	1.21
14951	0.02782	mioc9698	clone IMAGE:4820928, mRNA /gb=BC033530	BC033530	1.53
3264	0.02782	fcrb9450	TEA domain family member 4 (TEAD4), mRNA /cds=(164,1468) /gb=NM_003213 /gi=4507426	NM_003213	0.84
9806	0.02782	ncr3041	7k03e02.x1 NCI_CGAP_GC6 cDNA clone IMAGE:3443402 3', mRNA sequence /clone=IMAGE:3443402 /clone_end=3' /gb=BF056273	BF056273	1.20
13829	0.02782	miod7146	chromosome 5 clone CTB-73N10, complete sequence	AC008700	1.24
10782	0.02782	ncr4597	chromosome 15, clone RP11-815J21, complete	AC087286	1.18
14300	0.02782	mioc3413	twisted gastrulation 1 (Drosophila) (TWSG1), mRNA /cds=(106,777) /gb=NM_020648 /gi=21314788	NM_020648	1.24
13128	0.02782	fcrc4841	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12), mRNA /cds=(81,362)	NM_000609	0.69
8859	0.02782	seoc5863	clone IMAGE:5263177, mRNA /gb=BC035116	BC035116	1.68
10592	0.02782	mioc3492	activating transcription factor 1, clone MGC:32666 IMAGE:4102231, mRNA, complete cds	BC029619	1.18
14060	0.025999	ncr5027	beta-amyloid binding protein precursor (BBP), mRNA /cds=(304,927) /gb=NM_032027 /gi=17738309	NM_032027	0.80
10999	0.025999	miob7910	ax37a08.x1 Proliferating Erythroid Cells (LCB:ax library) cDNA clone ax37a08 random, mRNA	BG943384	1.24
4922	0.025999	ncrc0421	topoisomerase (DNA) II beta 180kDa (TOP2B), mRNA /cds=(1,4866) /gb=NM_001068 /gi=19913407	NM_001068	0.82
11985	0.025999	seoc4288	protocadherin beta 16 (PCDHB16), mRNA /cds=(1156,3486) /gb=NM_020957 /gi=14195604	NM_020957	1.21
8926	0.025999	ncr8652	clone IMAGE:5001859, mRNA /gb=BC040072	BC040072	1.24
4963	0.025999	ncrc6697	cytochrome c oxidase subunit VIIa polypeptide 2 (liver) (COX7A2), nuclear gene encoding mitochondrial protein, mRNA /cds=(76,327) /gb=NM_001865	NM_001865	0.77
14766	0.025999	mioc3059	cDNA FLJ30301 fis, clone BRACE2003217. /gb=AK054863 /gi=16549482 /ug=Hs.285728	AK054863	1.37
11259	0.025999	fcrc5160	actin binding LIM protein 1 (ABLIM1), transcript variant ABLIM-I, mRNA /cds=(100,2436) /gb=NM_002313	NM_002313	0.70
12371	0.025999	miob8685	BAC clone RP11-395A23 from 2, complete sequence	AC010149	1.31
13713	0.025999	mioc2592	heterogeneous nuclear ribonucleoprotein H2 (H') (HNRPH2), mRNA /cds=(79,1428) /gb=NM_019597	NM_019597	1.11
8278	0.025999	seoa6914	DNA sequence from clone RP3-414L4 on	AL139101	1.16
12248	0.025999	ncrb1544	12 BAC RP11-282K24 (Roswell Park Cancer Institute	AC092828	1.29
205	0.025999	ncr3016	mRNA for KIAA0268 gene, partial cds. /cds=(1,3582) /gb=D87742 /gi=1665824 /ug=Hs.241552 /len=5976	D87742	0.62
11048	0.024278	miod0611	genomic DNA, chromosome 18p clone:RP11-888D10,	AP001033	1.30
1574	0.024278	fcrb2380	similar to triple functional domain (PTPRF interacting) (LOC115557), mRNA /cds=(331,1755)	NM_133483	0.74

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4432	0.024278	ncr7227	no match		1.55
3861	0.024278	hfc0285	basigin (BSG), mRNA /cds=(58,867) /gb=NM_001728 /gi=4502458 /ug=Hs.74631 /len=1638	NM_001728	1.31
14835	0.024278	miod3154	BX115107 Soares fetal liver spleen 1NFLS cDNA clone IMAGp998G12373, mRNA sequence /clone=IMAGp998G12373; IMAGE:195875	BX115107	1.34
10669	0.024278	miod6984	DNA sequence from clone RP11-176D17 on	AL929236	1.32
1409	0.024278	seoa2042	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2 (KDEL2), mRNA	NM_006854	0.74
11585	0.024278	seoa1615	hypothetical gene supported by BC033907	XM_290641	1.22
9920	0.022655	miob9901	hypothetical protein FLJ22419 (FLJ22419), mRNA /cds=(409,1596) /gb=NM_024697 /gi=13375980	NM_024697	0.75
3005	0.022655	fcrb5926	likely ortholog of mouse Paneth cell enhanced expression (HCLA-ISO), mRNA /cds=(1152,2198)	NM_030937	0.83
13959	0.022655	seob5809	wi63d02.x1 NCI_CGAP_Kid12 cDNA clone IMAGE:2397987 3', mRNA sequence /clone=IMAGE:2397987 /clone_end=3' /gb=AI762877	AI762877	1.44
5402	0.022655	ncrc2135	cDNA FLJ39467 fis, clone PROST2012448	AK096786	0.83
14564	0.022655	fcr6948	mRNA for KIAA2019 protein. /cds=(15,8408) /gb=AB095939 /gi=24899201 /ug=Hs.57548 /len=9217	AB095939	1.37
1687	0.021125	ncrc6756	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein) (DBI), mRNA	NM_020548	0.80
7953	0.021125	ncr8320	UI-H-DP0-avb-i-09-0-UI.s1 NCI_CGAP_Fs1 cDNA clone IMAGE:5877200 3', mRNA sequence /clone=IMAGE:5877200 /clone_end=3' /gb=BQ020506	BQ020506	1.19
4271	0.021125	fcr4444	ras gene family, member E (ARHE), mRNA /cds=(141,875) /gb=NM_005168 /gi=21361257	NM_005168	0.74
13524	0.021125	seob5032	hypothetical protein DKFZp586C1924 (DKFZp586C1924), mRNA /cds=(106,693)	NM_032273	1.39
8553	0.021125	ncrc9434	DNA sequence from clone RP4-765C7 on	AL365357	1.19
6035	0.021125	miob6486	BCL2 gene, exon 3 and breakpoint region	AF217803	0.83
10860	0.021125	fcrb5299	mitochondrion, complete genome	NC_001807	0.83
2829	0.019683	seoa5239	mitochondrion, complete genome	NC_001807	0.81
14345	0.019683	mioc5633	mRNA; cDNA DKFZp586E1624 (from clone DKFZp586E1624) /gb=AL110152 /gi=5817054	AL110152	1.30
2175	0.019683	mioa4277	clone IMAGE:4799018, mRNA /gb=BC045722	BC045722	0.84
5222	0.019683	seoa9321	Saccharomyces cerevisiae chromosome XII, complete	NC_001144	0.77
12193	0.019683	ncr6368	trophoblast-derived noncoding RNA (TncRNA), misc	XR_000148	1.43
12780	0.019683	fcrc0106	mRNA; cDNA DKFZp434M2315 (from clone	AL133060	1.23
14760	0.019683	control	blank		1.21
14307	0.019683	mioc5129	alpha gene sequence	AF203815	1.37
2865	0.019683	seob2661	nudix (nucleoside diphosphate linked moiety X)-type motif 4 (NUDT4), mRNA /cds=(191,736)	NM_019094	0.88
5935	0.018325	mioa8902	MR2-CI0186-291100-010-a06 CI0186 cDNA, mRNA sequence /gb=BF814502 /gi=12147047	BF814502	1.33
11215	0.018325	miob2602	no match		1.39
13565	0.018325	ncr7556	clone RP11-299G20, complete sequence	AC023024	1.20
2088	0.018325	ncr5613	hypothetical protein LOC51257 (LOC51257), mRNA /cds=(352,1092) /gb=NM_016496 /gi=24475980	NM_016496	0.51

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Spot	p-value	Clone	Description	Accession	Allergies/No Allergies
12804	0.018325	seob7747	hypothetical protein FLJ38716 (FLJ38716), mRNA /cds=(266,1354) /gb=NM_152367 /gi=22748790	NM_152367	1.18
11876	0.018325	miod5301	immediate early response 3 (IER3), transcript variant long, mRNA /cds=(30,611) /gb=NM_052815	NM_052815	1.22
12109	0.018325	seob1922	clone IMAGE:5266665, mRNA, partial cds	BC036526	1.28
6148	0.018325	fcr5369	zinc finger RNA binding protein (ZFR), mRNA /cds=(44,1300) /gb=NM_016107 /gi=7706372	NM_016107	0.80
13074	0.018325	seoc6844	chromosome 5 clone CTB-46B19, complete sequence	AC011405	1.36
10407	0.018325	ncrc0992	clone IMAGE:125405, mRNA sequence /gb=AF339770 /gi=13507308 /ug=Hs.221635 /len=790	AF339770	0.61
12344	0.017049	fcrb8236	gm117 (gm117), mRNA	XM_086187	1.28
1445	0.017049	seoa9997	nuclear receptor coactivator 6 (NCOA6), mRNA /cds=(2755,8760) /gb=NM_014071 /gi=7661975	NM_014071	0.71
14494	0.017049	ncr3522	DNA sequence from clone RP11-460N11 on	AL359955	1.35
5235	0.017049	seob1399	major histocompatibility complex, class II, DR beta 1 (HLA-DRB1), mRNA /cds=(63,863) /gb=NM_002124	NM_002124	3.16
14324	0.017049	miod0452	chromosome 15, clone RP11-530L17, complete	AC022692	1.30
4020	0.017049	ncrb5704	CASP8 associated protein 2 (CASP8AP2), mRNA /cds=(197,6145) /gb=NM_012115 /gi=16306505	NM_012115	0.57
14763	0.017049	mioc2277	alpha gene sequence	AF203815	1.45
4125	0.017049	miob6087	for protein disulfide isomerase-related (PDIR), mRNA /cds=(57,1616) /gb=NM_006810 /gi=5803120	NM_006810	0.80
1836	0.017049	fcrc0775	hypothetical protein FLJ23445 (FLJ23445), mRNA /cds=(44,658) /gb=NM_025075 /gi=13376622	NM_025075	1.21
12429	0.015849	mioc3625	12 BAC RP11-114F3 (Roswell Park Cancer Institute	AC135279	1.26
3657	0.015849	fcrb5016	oxysterol binding protein-like 5 (OSBPL5), transcript variant 1, mRNA /cds=(117,2756) /gb=NM_020896	NM_020896	0.75
5071	0.015849	fcrb6619	cDNA FLJ10004 fis, clone HEMBA1000076. /gb=AK000866 /gi=7021190 /ug=Hs.411490 /len=1974	AK000866	0.75
7204	0.015849	fcrb3920	chromosome 20 open reading frame 98 (C20orf98), mRNA /cds=(134,748) /gb=NM_024958 /gi=13376446	NM_024958	1.14
4438	0.014722	ncr9460	BAC clone RP11-367I6 from 4, complete sequence	AC079257	1.30
14971	0.014722	fcrc1006	BAC clone RP11-427H3 from 2, complete sequence	AC114772	1.45
11002	0.014722	miob8640	AU119153 HEMBA1 cDNA clone HEMBA1005152 5', mRNA sequence /clone=HEMBA1005152 /clone_end=5' /gb=AU119153 /gi=10934388	AU119153	1.30
11025	0.014722	mioc3741	alpha gene sequence	AF203815	1.44
14717	0.013664	mioc0116	cDNA FLJ32589 fis, clone SPLEN2000443. /gb=AK057151 /gi=16552741 /ug=Hs.21342 /len=2178	AK057151	1.21
3719	0.013664	fcrb8202	putative ribonuclease III (RNASE3L), mRNA /cds=(246,4370) /gb=NM_013235 /gi=21359821	NM_013235	0.76
12120	0.013664	seob5143	mRNA; cDNA DKFZp761O0611 (from clone DKFZp761O0611) /gb=AL834155 /gi=21739631	AL834155	1.37
11637	0.013664	seob0767	genomic DNA, chromosome 11q clone:RP11-630P1,	AP002774	1.22
12941	0.012673	mioc5730	MR2-CI0186-291100-010-a06 CI0186 cDNA, mRNA sequence /gb=BF814502 /gi=12147047	BF814502	1.38
5749	0.012673	hfcr3486	up-regulated gene 4 (URG4), mRNA /cds=(14,2782) /gb=NM_017920 /gi=19923541 /ug=Hs.5131	NM_017920	1.25
12004	0.012673	mioa8526	chromosome 4 clone RP11-442P12, complete	AC005798	1.32

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5628	0.012673	fcr2088	v-fos FBJ murine osteosarcoma viral oncogene (FOS), mRNA /cds=(156,1298) /gb=NM_005252	NM_005252	3.33
2698	0.011744	mioa9792	topoisomerase (DNA) II alpha 170kDa (TOP2A), mRNA /cds=(127,4722) /gb=NM_001067	NM_001067	1.35
14884	0.011744	seob9125	602043661F1 NCI_CGAP_Brn67 cDNA clone IMAGE:4181462 5', mRNA sequence /clone=IMAGE:4181462 /clone_end=5' /gb=BF528488	BF528488	1.39
8577	0.010874	ncrc3050	RC5-FT0194-271100-022-B06 FT0194 cDNA, mRNA sequence /gb=BF858635 /gi=12246379	BF858635	1.25
12897	0.010874	mioc3745	alpha gene sequence	AF203815	1.40
3979	0.010874	ncrb3329	TGFB inducible early growth response (TIEG), mRNA /cds=(124,1566) /gb=NM_005655 /gi=5032176	NM_005655	0.50
12489	0.010874	miod0781	MR2-CI0186-291100-010-a06 CI0186 cDNA, mRNA sequence /gb=BF814502 /gi=12147047	BF814502	1.48
12541	0.010874	miod7022	yb61c11.s1 Stratagene ovary (#937217) cDNA clone IMAGE:75668 3', mRNA sequence	T58438	1.29
11024	0.010874	mioc3523	hypothetical protein MGC33607 (MGC33607), mRNA /cds=(42,2543) /gb=NM_152775 /gi=22749514	NM_152775	1.36
11898	0.010874	mioc7471	intersectin 2 (ITSN2), transcript variant 1, mRNA /cds=(242,5332) /gb=NM_006277 /gi=22325384	NM_006277	1.39
3143	0.010061	seob8212	hypothetical protein FLJ20671 (FLJ20671), mRNA /cds=(43,465) /gb=NM_017924 /gi=19923511	NM_017924	0.80
13992	0.010061	seoa4338	DNA sequence from clone RP4-657E11 on chromosome 1p35.1-36.23, complete sequence	AL035413	1.42
6758	0.010061	ncrc0393	proteasome (prosome, macropain) 26S subunit, ATPase, 2 (PSMC2), mRNA /cds=(71,1372)	NM_002803	0.81
9454	0.009301	mioc0238	praja 1 (PJA1), mRNA /cds=(295,1662) /gb=NM_022368 /gi=21539662 /ug=Hs.21122	NM_022368	0.66
5701	0.008591	hfcr0967	mitochondrion, complete genome	NC_001807	0.75
6097	0.008591	fcr2293	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide (YWHAG), mRNA /cds=(192,935)	NM_012479	0.68
3181	0.007929	fcrb3476	protein phosphatase 2A, regulatory subunit B' (PR 53) (PPP2R4), mRNA /cds=(190,1161) /gb=NM_021131	NM_021131	0.77
6866	0.007929	ncrc5959	E1A binding protein p300 (EP300), mRNA /cds=(1200,8444) /gb=NM_001429 /gi=4557556	NM_001429	0.86
14504	0.007929	fcr2881	no match		1.43
13282	0.007929	miod5682	LIS1-interacting protein NUDEL; endooligopeptidase A (NUDEL), mRNA /cds=(134,1171) /gb=NM_030808	NM_030808	1.34
6238	0.007929	miod3414	tb97a11.x1 NCI_CGAP_Co16 cDNA clone IMAGE:2062268 3' similar to contains Alu repetitive element; mRNA sequence /clone=IMAGE:2062268	AI343476	0.56
5258	0.007312	seob5658	testis derived transcript (3 LIM domains) (TES), transcript variant 1, mRNA /cds=(182,1447)	NM_015641	0.73
11823	0.007312	miob8896	mRNA for KIAA1614 protein, partial cds. /cds=(1,3628) /gb=AB046834 /gi=10047302	AB046834	1.24
8818	0.006737	seoc4234	Similar to KIAA1753 protein, clone IMAGE:5210724, mRNA /gb=BC033751 /gi=21707446 /ug=Hs.44976	BC033751	0.58



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Spot	p-value	Clone	Description	Accession	Allergies/No Allergies
6065	0.006737	seoa4327	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa (NDUFC2), mRNA	NM_004549	0.82
5639	0.006202	fcr4328	mitogen-activated protein kinase 7 (MAPK7), transcript variant 1, mRNA /cds=(355,2805)	NM_139033	0.81
12542	0.006202	miod7462	chromosome 8, clone RP11-520P18, complete	AC083982	1.50
3492	0.006202	ncrc1867	UI-H-BI2-ags-a-03-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2725156 3', mRNA sequence /clone=IMAGE:2725156 /clone_end=3'	AW292521	1.30
8104	0.006202	mioc3797	mRNA; cDNA DKFZp761C169 (from clone DKFZp761C169); partial cds /cds=(997,2475)	AL161991	1.28
2866	0.005705	seob2937	translation initiation factor IF2 (IF2), mRNA /cds=(142,3804) /gb=NM_015904 /gi=15451891	NM_015904	0.82
8519	0.005705	fcrb2886	AGENCOURT_6423660 NIH_MGC_67 cDNA clone IMAGE:5580917 5', mRNA sequence /clone=IMAGE:5580917 /clone_end=5' /gb=BM465996	BM465996	1.40
4834	0.005243	seob6878	mitochondrion, complete genome	NC_001807	0.75
7656	0.005243	mioc8607	cDNA FLJ35517 fis, clone SPLEN2000698. /gb=AK092836 /gi=21751529 /ug=Hs.291804	AK092836	1.41
7227	0.005243	ncrc0572	cytidine monophosphate kinase CMP mRNA, (=UMP-phosphatidylinositol-3 phosphate 3-phosphatase adaptor subunit (3PAP), mRNA /cds=(132,2375)	AF259961.1	0.80
8310	0.005243	miob3072	phosphatidylinositol-3 phosphate 3-phosphatase adaptor subunit (3PAP), mRNA /cds=(132,2375)	NM_019061	1.42
11870	0.004814	miod4154	clone 114 tumor rejection antigen mRNA, complete cds /cds=(3482,3544) /gb=AF445027 /gi=17386079	AF445027	1.44
6068	0.004417	seoa4802	mitochondrial ribosomal protein L27 (MRPL27), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA /cds=(32,316)	NM_148571	0.79
4738	0.004417	seob2938	nuclear factor I/A (NFIA), mRNA	XM_046827	0.79
3173	0.004048	ncrc9642	hypothetical protein FLJ11730 (FLJ11730), mRNA /cds=(33,608) /gb=NM_022756 /gi=20149668	NM_022756	0.81
4853	0.003707	fcrb2558	clone 24571 mRNA sequence /gb=AF070564	AF070564	0.66
10798	0.003707	ncrb7230	12 BAC RP11-474P2 (Roswell Park Cancer Institute	AC025031	1.24
7763	0.003707	seoc1508	chromosome 21 open reading frame 6 (C21orf6), mRNA /cds=(92,1051) /gb=NM_016940 /gi=8393017	NM_016940	0.84
7762	0.003101	seoc1356	Similar to ubiquitin protein ligase E3A papilloma virus E6-associated protein, Angelman syndrome), clone IMAGE:4811444, mRNA /gb=BC040187	BC040187	0.80
14924	0.002584	miob4872	no match		1.49
13913	0.002356	mioa8749	DNA sequence from clone RP11-427L15 on	AL139407	1.36
12624	0.001952	ncr8248	12 BAC RP13-501J24 (Roswell Park Cancer Institute	AC122687	1.96
6865	0.001774	ncrc5780	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4), mRNA	NM_002489	0.79
8647	4.68E-04	fcrc3336	tm62d04.x1 NCI_CGAP_Brn25 cDNA clone IMAGE:2162695 3', mRNA sequence /clone=IMAGE:2162695 /clone_end=3' /gb=AI475033	AI475033	1.63
5079	3.76E-04	fcrb7324	APR-1 protein (MAGEH1), mRNA /cds=(271,930) /gb=NM_014061 /gi=18105051 /ug=Hs.279819	NM_014061	0.51